marker protein was not distinctly expressed in other cancers of the brain, breast, prostate, small intestine, stomach, and uterus or in normal or diseased bone, heart, muscle, or neurons.

Please amend the second paragraph on page 17, beginning on line 13 to recite:

Detection and quantification of a protein using either labeled amino acids or specific polyclonal or monoclonal antibodies are known in the art. Examples of such techniques include two-dimensional polyacrylamide gel electrophoresis, enzyme-linked immunosorbent assays (ELISAs), radioimmunoassays (RIAs), and fluorescence activated cell sorting (FACS). These assays and their quantitation against purified, labeled standards are well known in the art (Ausubel, supra, unit 10.1-10.6).

IN THE CLAIMS

Please cancel claims 13-20 without prejudice and consider new claims 21-23.

Please amend claims 2 and 7 as shown in the **"VERSION WITH MARKINGS TO SHOW CHANGES MADE"**.

For the Examiner's convenience, all pending claims are shown below.

1. An isolated cDNA comprising a nucleic acid sequence encoding a protein having the amino acid sequence of SEQ ID NO:1, and the complement of the cDNA.

2. (Once Amended) An isolated cDNA comprising a nucleic acid sequence selected from:

a) SEQ ID NO:2 and the complement of SEQ ID NO:2; and

b) a fragment of SEQ ID NO:2 selected from SEQ ID NOs:3-8 and the complements of SEQ ID NOs:3-8.

3. A composition comprising the cDNA of claim 1 and a labeling moiety.

4. A vector comprising the cDNA of claim 1.

5. A host cell comprising the vector of claim 4.

6 A method for using a cDNA to produce a protein, the method comprising:

a) culturing the host cell of claim 5 under conditions for protein expression; and

b) recovering the protein from the host cell culture.

7. (Once Amended) A method for using a cDNA to detect expression of a nucleic acid in a sample comprising:

a) hybridizing the composition of claim 3 to nucleic acids of the sample under conditions to form hybridization complexes; and

b) detecting hybridization complex formation, wherein complex formation indicates expression of a nucleic acid complementary to the cDNA of the composition in the sample.

8. The method of claim 7 further comprising amplifying the nucleic acids of the sample prior to

hybridization.

9. The method of claim 7 wherein the composition is attached to a substrate.

10. The method of claim 7 wherein complex formation is compared with at least one standard to determine differential expression.

11. A method of using a cDNA to screen a plurality of molecules or compounds, the method comprising:

a) combining the cDNA of claim 1 with a plurality of molecules or compounds under conditions to allow specific binding; and

b) detecting specific binding, thereby identifying a molecule or compound which specifically binds the cDNA.

12. The method of claim 11 wherein the molecules or compounds are selected from DNA molecules, RNA molecules, peptide nucleic acids, artificial chromosome constructions, peptides, transcription factors, repressors, and regulatory molecules.

21. (New) The method of claim 11 wherein the cDNA is attached to a substrate.

a5 22. (New) The method of claim 10 wherein differential expression is diagnostic of cancer.

23. (New) The method of claim 22 wherein the cancer is selected from lymphoma, transitional cell carcinoma of the bladder, metastatic adenocarcinoma of the colon, Wilm's tumor, renal cell carcinomas, metastatic endometrial cancer, and testis tumor.